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2: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*

3: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*

4: /cgn2 6/ptodata/2/ina/PcTUS_COMB.seq:*

5: /cgn2 6/ptodata/2/ina/PcTUS_COMB.seq:*

6: /cgn2 6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          - nucleic search, using sw model
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mmmin-	11.1 665 11.1 640681 10.9 6243 10.9 19233 10.8 11131 10.8 5108 10.7 86952	26677		ion US ing, M ing, M wen N: Ro ES: 9 DRESS: neth D ffice e	DRM: PPY COM PC In R DAT	in i	Similarity 100 6; Conservative	SAAACATATTCAA?
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-08-883-795A-36 -07-872-678A-36 -10-204-708-6 -08-998-416-683	10-204-708-2 10-204-708-2 09-790-988-1 10-204-708-46 10-204-708-46 10-204-708-27 10-204-708-27 10-204-708-32	-08-446-855A-1 -09-150-741-1 -08-487-826B-13 -09-641-638-651	ALIGNMENTS	x Specific Gene; Bell, Seltzer,	e S-DOS #1.0, Version #1.3 508,786	65 5051-294 N:	Score 456; DB 2; Pred. No. 7.8e-86; ; Mismatches 0;	STAGTTTGCTACTCATAAT
Sequence 36, Appl Sequence 36, Appl Sequence 6, Appl Sequence 683, Appl Sequence 36, Appl	Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 46, Appli Sequence 27, Appl Sequence 8, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli	464		Promoter Park &	0		Length 1030; Indels 0; Gaps	GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATGGCTAGAATACTTTGTGCCTT 

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181 ATGAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA 240
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GENERAL INFORMATION:
APPLICANT: CONKING, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPENDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &
                                                                 ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: PCT/US96/12158
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456
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NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-294
TELECHMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post Office Drawer 34009
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE:
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PCT-US96-12158-5
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100.0%; Score 456; DB 5; Length 1030;

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                    Indels
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APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
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 red. No. 7.8e-86;
Mismatches 0;
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   Pred. No.
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CLASSIFICATION: 800
ATTORNEY/AGENT INPORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEFAK: 919-801-3175
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1294 base pairs
   ilarity 100.0%; P. Conservative 0;
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12158
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              685 CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG 720
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                                                                                            Score 456; DB 2;
Pred. No. 7.9e-86;
                                                                            100.0%; Scor.
100.0%; Pred. No. /...
0; Mismatches
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NAME: Sibley, Kerneth D. 665
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US96-12158-4; Sequence 4, Application PC/TUS9612158; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Conkling, Mark A. APPLICANT: Mendu, Nandini APPLICANT: Song, Wen TITLE OF INVENTION: ROOT COTTE OF NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-508-786-4
                                                                                            Query Match
Best Local Similarity 100.
Matches 456; Conservative
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APPLICANT: Conkling, Mark A.
APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &
ADDRESSEE: Gibson
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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100.0%; Score 456; DB 5;
Best Local Similarity 100.0%; Pred. No. 7.9e-86;
Matches 456; Conservative 0; Mismatches 0;
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STATE: No. 5837876th Carolina
TELECOMMUNICATION INFORMATION TELEPHONE: 919-420-2200 TELEFAX: 919-881-3175
                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                   TELEPRA: 919-420-2200
TELEPRA: 919-881-3175
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 11294 base pairs
                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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US-08-508-786-3
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APPLICATION NUMBER: US/08/508,786
FILING DATE:
CLASSIPTCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-294
TELECOMMUNICATION INFORMATION:
TELEFRYENCE, 919-420-2200
TELEFRY: 919-881-3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic) US-08-508-786-3
                                                                                                                                                                                                           LENGTH: 1372 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 456; Conservative
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STATE: North Carolina
COUNTRY: USA
ZIP: 28234
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US-08-508-786-2
Squence 2, Application US/08508786
Fatent No. 5837876
GENERAL INFORMATION:
APPLICANT: Conkling, Mark A.
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter;
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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100.0%; Score 456; DB 5; I
Best Local Similarity 100.0%; Pred. No. 8e-86;
Matches 456; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEFRONE: 919-420-220
TELEFRAX: 919-481-3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER.SIICS:
LENGTH: 1372 base pairs
TYPE: nucleic acid
STRANEBNESS: single
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MOLECULE TYPE: DNA (genomic)
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ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park
ADDRESSEE: Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
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                                                                                                   ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYREE Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 456; DB 2;
Pred. No. 8.2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 456; D
Best Local Similarity 100.0%; Pred. No. 8.2
Matches 456; Conservative 0; Mismatches
                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SIDLEY, KENDELD D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-480-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 base pairs
                                                                  No. 5837876th Carolina: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: DNA (genomic) US-08-508-786-2
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                     STATE: No COUNTRY:
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Sequence 2, Application PC/TUS9612158 GENERAL INFORMATION:

PCT-US96-12158-2

1259 AATTATCGGTACAGTTATAGATTTATAAAAATCTACGGTTCTTCAGAAGAAACTAAA 1318 121 ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC 180 61 GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA 120 361 AATCGGTTCGGTGCGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT 241 TITAATCGGTATAGTTCGATATTTTTTTTTTTTTATAAAATAAAAACTTACCCT 301 AATTATCGGTACAGTTATAGATTTATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA 1 GGAAACATATTCAATACATTGTAGTTTGCTACTACATAATCGCTAGAATACTTTGTGCCTT 181 ATGAAAATTTTAATGCTTTTAAACTTACTTATAAATTTTTCATATGTAAAA Gaps ö Indels 1379 ccraerrerrerraraegraaaagcaerracagae 1414 COMPUTER: IBM PC COMPALATION CONFIDENCE SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 Score 456; DB 5; Pred. No. 8.2e-86; Mismatches 0; APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer,
ADDRESSEE: Gibson SOFTWARE: Patentin Release #1.0, Vornern Application DATA:
APPLICATION NUMBER: PCT/US96/12158 STREET: Post Office Drawer 34009 CITY: Charlotte STATE: North Carolina COUNTRY: USA ATTORNEY/AGENT INFORMATION:
NAME: SIBLEY, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-481-3175 ; 0 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible Query Match 100.0%; Best Local Similarity 100.0%; Matches 456; Conservative 0 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) LENGTH: 1988 base pairs TYPE: nucleic acid STRANDEDNESS: single INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: FILING DATE: CLASSIFICATION: 28234 PCT-US96-12158-2 421 셤 ò

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ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION UNMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-
TELECOMMUNICATION INFORMATION:
TELEFONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-12158-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2010 base pairs
                                                                                                                                                                                                                                                                                                                                        CITY: Charlotte
STATE: North Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 456; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                          PCT-US96-12158-1
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                                                             GENERAL INFORMATION:
APPLICANT: Conkling, Mark A.
APPLICANT: Conkling, Mark A.
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &
ADDRESSEE: Gibson
STREET: Post Office Drawer 34009
                                                                                                                                                                                                                                                                                  ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 456; DB 2; Best Local Similarity 100.0%; Pred. No. 8.2e-86; Matches 456; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                  STREET: Post Office Drawer 340 CITY: Charlotte STATE: No. 5837876th Carolina COUNTRY: USA
                                 Sequence 1, Application US/08508786
Patent No. 5837876
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/ACENT INFORMATION:
NAME: SIBLEY, Kenneth D.
REGISTRATION NUMBER: 31665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-481-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TENGTH: 2010 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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US-08-508-786-1
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361 AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT 420
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                                                                                                                                                                                                                                                                                                                                                                    Root Cortex Specific Gene Promoter
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: CONKING, Mark A.
APPLICANT: CONKING, Mandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promote
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gibson
STREET: Post Office Drawer 34009
                                                                                                                    CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: PCT/US96/12158
FILING DATE:
                                                                                       421 CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG 456
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100.0%; Pred. No. 8.2e-86;
Live 0; Mismatches 0;
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                                                                          1319 AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT 1378
1199 TTTAATCGGTATAGTTCGATATTTTTTTAATTTTTTTAAAATAAAAAAACTTACCCT 1258
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                                            301 AATTATCGGTACAGTTATAGATTTATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA 360
                                                                                                                               361 AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Conkling, Mark A.

APPLICANT: Mendu, Nandini
APPLICANT: Song, War
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &
ADDRESSEE: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTINUES TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SIDLEY, Kenneth D.
REGISTRATION NUMBER: 31,665
REFRENCE/DOCKET NUMBER: 5051-294
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                        1379 CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG 1414
                                                                                                                                                                                                                          421 CCTAGTTGTTGTTATAGGTAAAAGCAGTTACAGAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 TIGITATAGGTAAAAGCAGTTACAGAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abunan
STRET: Post var-
CITY: Charlotte
STATE: No. 5837876th Carolina
                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08508786
Patent No. 5837876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 72 base pairs TYPE: nucleic acid STRANDEDNESS: single CONCOUNTY TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-508-786-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 919-881-3175
                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-508-786-6
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369 CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG 428
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0
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                                            APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &
ADBRESSEE: Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: North Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NAME: PCT/US/NS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFRENCE/POCKET UNBER: 5051-294
TELECOMMUNICATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 148; DB 5; 1
100.0%; Pred. No. 2.2e-22;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 288, Application US/08998416; Patent No. 6239264; GENERAL INFORMATION: APPLICANT: Philippsen, Peter APPLICANT: Pohlamann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Wohr, Christine APPLICANT: Wendland, Jurgen APPLICANT: Knechle, Philipp APPLICANT: Rebischung, Corinne
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 6, Application PC/TUS9612158
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERICSTICS:
LENGTH: 722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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Matches 148; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           ZIP: 28234
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NAME/KEY: misc feature
LOCATION: 1123.3123
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 3124.3297
OTHER INFORMATION: exon 1
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LOCATION: 3871..4072
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5996..6099
OTHER INFORMATION: exon 5
LOCATION: 6349..6509
OTHER INFORMATION: exon 5
LOCATION: 6349..6509
OTHER INFORMATION: exon 5
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
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OTHER INFORMATION: exon 10
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OTHER INFORMATION: exon 11
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OTHER INFORMATION: exon 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 12254..12340
OTHER INFORMATION: exon 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AGTATTITGAGTTTAATTACTTATTG--ACTTGTAACAGTTTTTATAATTCCAAGGCCCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 TGAAAATITTAATGCTITTATTAGTTTTAAACTTACTATAAATTTTTCATATGTAAAAT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 TAAATATTATGTTGATTTATTTTAATCTTTTTATAAGAATTATTAAAAATTAAT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAATCGGTATAGTTCGATATTTTTTCAATTTTTTTTTAAAATAAAAAACTTACCCTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trraactrraatrrictratratratrrratatratratataaratatatricatrria 533
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                      GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
AND USES THEREOF
1152
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Best Local Similarity 51.1%; Pred. No. 0.00023;
Matches 168; Conservative 0; Mismatches 159; Indels
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GY
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 623264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP 27706
COMPUTER: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CUMBENT APPLICATION NUMBER: US/08/998,416
FILING DATE: 31-DEC-1997
CLASSIFICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-199
CLASSIFICATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELEPAN: 919-541-8689
INFORMATION FOR SEQ ID NO: 288:
SEGUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TTELEFAN: 919-541-8689
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TTELEFAN: 919-641-8689
INFORMATION FOR SES ID NO: 288:
TELENGTH: 837 base pairs
TTELEFAN: 919-641-8689
INFORMATION FOR SES ID NO: 288:
TRANDEDNESS: saingle
TODOTOGY INFORMATION
TTELEFANS: 919-641-8689
INFORMATION FOR SES ID NO: 288:
TRANDEDNESS: saingle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-641-638-651
; Sequence 651, Application US/09641638
; Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAG1241RP
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APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
CURRENT FILING DATE: 2000-00-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-21
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 1304
SSOFIWARE: Patent.pm
LENGTH: 20674
TENGTH: 20674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 17063..17554
OTHER INPORMATION: excn 14
NAME/KEY: misc.feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
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ic base C or T ic base C or T ic base C or T	motif ATTTA or TTTTTT c base C or T .c base G or C ic base A or G	c base A or c base C or c base A or c base A or base A or	of C iic base C or T iic base C or T iic base G or T	ic base A or G ic base G or C ic base C or T c base A or G ic base G or C
<ul><li>polymorphic</li><li>polymorphic</li><li>polymorphic</li><li>deletion of</li></ul>	<ul><li>variable m</li><li>polymorphic</li><li>insertion</li><li>polymorphic</li><li>polymorphi</li></ul>	H	<pre>: deletion of : polymorphic : polymorphic : polymorphic : polymorphic</pre>	: polymorphic : polymorphic : polymorphic : polymorphic } : polymorphic
10-508-191 10-508-245 10-509-284 10-509-295	10-510-173 10-511-62 10-511-337 10-512-36 10-512-318	-513-26 -513-26 -513-35 -513-36	10-343-231 12-206-366 10-343-278 10-346-23	10-346-141 10-346-263 10-346-305 10-347-74 10-347-111
NAME/KEY: allele LOCATION: 1128 OTHER INFORMATION: NAME/KEY: allele LOCATION: 1182 OTHER INFORMATION: NAME/KEY: allele LOCATION: 1559 OTHER INFORMATION: NAME/KEY: allele LOCATION: 1570 COTHER INFORMATION: NAME/KEY: allele	0 0 0 0	XH XH XH XH XH XI	CTHER INFORMATION: NAME/KEY: allele LOCATION: 4088 LOCATION: 4088 COTHER INFORMATION: NAME/KEY: allele LOCATION: 4170 OTHER INFORMATION: OTHER INFORMATION: NAME/KEY: allele LOCATION: 5903 OTHER INFORMATION: NAME/KEY: allele LOCATION: 5903 OTHER INFORMATION: NAME/KEY: allele LOCATION: 5003	OTHER INFORMATION: NAME/KEY: allele LOCATION: 6141 COCATION: 6183 OTHER INFORMATION: NAME/KEY: allele LOCATION: 6338 OTHER INFORMATION: NAME/KEY: allele LOCATION: 6375 OTHER INFORMATION: NAME/KEY: allele LOCATION: 6375 OTHER INFORMATION:

11184 AATTTAAATAAATTTAAATTTAAAATTTAATTTTAATTTAAATAAACATTTAAATTTT 11243 11064 TTTTTAATAGCTAAGGAAAHATTTTAATTTTTAATTTTAATATTTTAATTTTAATTTAATT 11123 111 GATTTTAGGAATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAAT 170 171 TCCAAGGCCCATGAAAATTTAATGCTTTAATTAAACTTTACTATATAAATTTTTC 230 Gaps .; 0 Length 20674; Score 59.4; DB 4; Length 20 Pred. No. 0.00054; 0; Mismatches 156; Indels or C : polymorphic base C or T H : polymorphic base C or T Ö Ö Ö : polymorphic base G or C H : polymorphic base A or G : polymorphic base A or G : polymorphic base A or : polymorphic base C or : polymorphic base A or : polymorphic base A or : polymorphic base A or : polymorphic base A or : polymorphic base G or : polymorphic base C or : polymorphic base C or : polymorphic base C or : polymorphic base A : deletion of CTG NAME/KEY: allele
LOCATION: 13341
LOCATION: 13441
LOCATION: 13492
LOCATION: 13492
LOCATION: 13524
LOCATION: 13524
LOCATION: 13524
LOCATION: 13524
LOCATION: 13524
LOCATION: 13533:
NAME/KEY: allele
LOCATION: 13534 NAME/KEY: allele
LOCATION: 8777
COTHER INFORMATION: 10-349-216:
NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224:
NAME/KEY: allele
LOCATION: 8926
OTHER INFORMATION: 10-349-368: LOCATION: 6611
OTHER INFORMATION: 10-347-348:
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391:
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47: NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 :
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 INFORMATION: 10-347-165 NAME/KEY: allele LOCATION: 12429 OTHER INFORMATION: 10-350-332 LOCATION: 6534 OTHER INFORMATION: 10-347-271 NAME/KEY: allele Query Match
Best Local Similarity 49.5%;
Matches 153; Conservative LOCATION: 6467 OTHER INFORMATION: 10-347-203 LOCATION: 6484 OTHER INFORMATION: 10-347-220 NAME/KEY: allele LOCATION: 12171 OTHER INFORMATION: 10-350-72 NAME/KEY: allele 231 qq g à 셤 ò 셤 ò δ

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Sequence 3, Application US/09801861
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; TITLE ON INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3;
LENGTH: 53332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31283 TAATAATAATTCTAAAAATGGCAATCACGTATATATTTTTATATATTTTTTATAT 31342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 TAAAGATACTTGAAATAGCTTAGTTTAAATATAACATAATAGATTTTAGGAATTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 AAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 TCGGTATAGTTCGATATTTTTCAATTTATTATAAAAAACTTACCCTAATTA 305
291 AACTTACCCTAATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.5%; Score 57; DB 4; Length 53332; Best Local Similarity 49.8%; Pred. No. 0.0018; Matches 144; Conservative 0; Mismatches 145; Indels
                                                                                                               11364 TTAATTTAA 11372
                                                                           351 GAAACCTAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3
                                                                                                                                                                              RESULT 15
US-09-801-861-3
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Search completed: August 3, 2004, 19:58:48 Job time : 68 secs

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August 3, 2004, 19:52:20 ; Search time 339 Seconds (without alignments) 6595.374 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/PCT_RBW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_RBW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/BCG_NBW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NBW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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15: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3222919 seqs, 2451570024 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               sw model
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                                                                                                                                               nucleic search, using
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Maximum DB seq length: 2000000000
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456
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Sequence:
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                                                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		φp				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	456	100.0	456	13	US-09-941-042C-1	Sequence 1, Appli
N	456	100.0	456	17	US-10-363-069-1	Sequence 1, Appli
m	9.99	14.6	5145	15	US-10-311-455-321	Sequence 321, App
4	9.99	14.6	5145	15	US-10-240-485-17	Sequence 17, Appl
S	66.4	14.6	8305	15	US-10-311-455-1541	Seguence 1541, Ap
9	61	13.4	6175	15	US-10-311-455-1280	Sequence 1280, Ap
C 7	61	13.4	158001	17	US-10-211-179-11	GENERAL INFORMATI
80	60.4	13.2	18997	15	US-10-172-086-17	Sequence 17, Appl
9	60.4	13.2	18997	15	US-10-311-455-543	Sequence 543, App
10	60.4	13.2	18997	17	US-10-311-507-31	Sequence 31, Appl
11	60.2	13.2	5925	15	US-10-311-455-1549	Sequence 1549, Ap
12	9	13.2	8305	15	US-10-311-455-1542	Sequence 1542, Ap
13	59.6	13.1	5407	15	US-10-311-455-2064	Sequence 2064, Ap
14	59.4	13.0	20674	16	US-10-170-097-651	Sequence 651, App

THEORY TINEORMANT	Company 7035 An			$^{\circ}$	50,	68,	1,	518,		2102		1564		201,	39,	71,	Sequence 2108, Ap	н.	Sequence 3, Appli	Sequence 3, Appli	4, A	226	32,		28,	598	863,	Sequence 214, App	2126	73	Sequence 115, App
04, 1,00	US-10-211-119-11		US-10-240-454-30	US-10-311-455-1422	US-10-221-613-50	US-10-240-485-68	us-	US-10-221-714A-518	US-10-172-086-50	US-10-311-455-2102	US-10-311-507-20	US-10-311-455-1564	US-10-240-589C-86	US-10-221-714A-201	US-10-172-086-39	US-10-311-507-71	US-10-311-455-2108	US-10-257-166-120	US-09-801-861-3	US-10-224-562-3	US-10-300-611-4	US-10-221-613-226	US-10-221-714A-32	US-10-311-455-334	US-10-240-485-28	US-10-311-455-598	US-10-311-455-863	US-10-240-453-214	US-10-311-455-2128	_	US-10-240-589C-115
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	TARRET	858	8842	8842	6062	8197	3673778	6050	6050	6050	6050	10279	10279	8085	8085	8085	10886	16258	53332	53332	91352	6013	6095	6095	6095	16217	6131	6631	15548	5152	5152
	7.7	12.8	12.8	12.8	12.7	12.7	12.7	12.6	12.6	12.6	12.6	12.6	12.6	12.5	12.5	12.5	12.5	12.5	12.5	12.5	12.5	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.3	12.3
(	, ה ה	58.2	58.2	58.2	25	ı cr	200	57.6	57.6	57.6	57.6	57.6	57.6	57.2	57.2	57.2	57	57	57	57	56.8	56.6	56.6	9.99	9.99	9.99	56.4	56.4	56.4	56.2	56.2
,	T?	16	17	18	19	10	21	22	23	24	25	56	27	28	29	30	31	32	8	34	35	36	37	38	39	40	41	4	43	44	45
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICATION O. US20030018997A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CONTAINING MOLECULAR DECOYS THAT ALTER PROTEIN
TITLE OF INVENTION: TREREIN
FILE REFERENCE: 5051-471W0
CURRENT FILING DATE: 2002-08-20
CURRENT FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PALENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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                                                                                                                                                                                                                                                                                                                            ORGANISM: Nicotiana tabacum
US-09-941-042C-1
US-09-941-042C-1
                                                                                                                                                                                                                                                                                               LENGTH: 456
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                              SEQ ID NO 1
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by Determ

Oy 361 AATCGGTTCGGTCCGGACGTTCGATTGGTTTTCAAATATTCATTGACGT 420	PRIOR FILING DATE: 2000-07-02  PRIOR FILING DATE: 2000-06-30  PRIOR APPLICATION NUMBER: DE 10043826.1  PRIOR PILING DATE: 2000-09-01  PRIOR PILING DATE: 2000-09-01  PRIOR PILING DATE: 2000-09-01  PRIOR PILING DATE: 2000-09-01  CONGANISM: Artificial Sequence  PEATURE: DNA  PEATURE: DNA  CORGANISM: Artificial Sequence  PEATURE: DNA  CORGANISM: Artificial Sequence  PEATURE: DNA  PEATURE: DNA  CORGANISM: Artificial Sequence  PEATURE: DNA  PEATURE: DN		OY 184 AAAAATTAAAIGCTTTATAGTTTTAAACTTACTATATAAATTTTCATATGTAAAATTT 243	Oy 304 TATCGGTACAGTTATATAAAAATCTACGGTT 342
Oy 181 ATGAAAATTTAATGCTTTATTAAACTTACTATAAAATTTTCATATGTAAA 240  Db 181 ATGAAAATTTAATGCTTTATTAAACTTACTATTAAAATTTTCATATGTAAA 240  Oy 241 TTTAATGGTATAGTTGATATTTTTTCAATTTATTAAAATAAAT	sequence 1, Application No. US/10363069  GENERAL INFORMATION: APPLICANT: Conviling, Mark A. APPLICANT: Conviling, Mark A. TITLE OF INVENTION: CONTENT THEREIN FILLE REFERENCE: 5051-471XX CURRENT FILLNG DATE: 2003-02-28 FRIOR PILING DATE: 2003-02-28 FRIOR PELING DATE: 2000-08-30 FRIOR PILING DATE: 2000-08-30 FRIOR PILING DATE: 2000-08-30 FRIOR PILING DATE: 2000-08-30 FRIOR PILING DATE: 2000-08-30 FRIOR PILING DATE: 2000-08-30 FRIOR PILING DATE: 2000-08-30 FRIOR FILING DATE: 2000-08-3	Query Match  Best Local Similarity 100.0%; Pred. No. 1.2e-69;  Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy   GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT 60	Qy         61 GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATAAATA	OY 181 ATGAAAATTTAATGCTTTATTAAACTTACTATATAAATTTTCATATGTAAAA 240  181 ATGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTCATATGTAAAA 240  181 ATGAAAAATTTAATGCTTTATTAGTTTTTATAAATTAAAAAAAA

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TITLE OF INVENTION: Observed of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR PRILING DATE: 2001-07-02
PRIOR PILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 AAGATACTTGAAATAGCTTAGTTTAAATATAAGCATAATAGATTTTAGGAATTAGTA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 ATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTTAATC
                                                                                                                                                                                                                                                                                                                                          8 TATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 GGTACAGTTATAGATTTATATAAAATCTACGGTTCTTCAGAAGAAACCTAAAAAT 363
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                                                                                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1541
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                                                                                                                                                                                                                                         Length 8305;
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Pred. No. 0.43;
0, Mismatches 175, Indels
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                            Score 66.4; DB 15;
Pred. No. 0.056;
0; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1280, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 48.7%;
Matches 166; Conservative
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 49.2%;
Matches 175; Conservative
                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2424
     PRIOR FILING DATE: 2000-09
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1541
LENGTH: 8305
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                                                                                                                                                   FEATURE:
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APPLICANT: PIEPENSENCE, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosia of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION WINBER: US/10/311,455
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAAAGATACTTGAAATAGCTTAAATATAAATAGCATAATAGATTTTAGGAATT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AATCGGTATAGTTCGATATTTTTTCAATTTATTTTTTTAAAATAAAAACTTACCCTAAT 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 AATATATTATAAGTTTTAATATTTTTTTTTTTTTATTTTATTTTGGGTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 TAİGTITAİGAGGGATAİATAİTITAAİTAAİTITAAİGIGLITITITITİTİTAATITİG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAATTTAATGCTTTAATTAGTTTTAAAACTTACTATATAAATTTTTCATATGTAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-485-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5145,
APPLICANT: 'PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007
GURRENT APPLICATION NUMBER: US/10/240,485
CURRENT PILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03970
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
SRIOR PILING DATE: 2000-09-01
SRIOR PILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 TATCGGTACAGTTATAGATTTATATAAAAATCTACGGTT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTGTTTTTAAAATATTGTAGTATATAAATTTÄTAGTT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66.6; DB 15;
Pred. No. 0.044;
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Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.9%;
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-10-311-455-1541/c
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Sequence 543, Application US/10311455
Fublication No. US20030143606A1
GENERAL INFORMATION:
GENERAL INFORMATION:
HOBICANT: PIEERBRECK, Christian
APPLICANT: PIEERBRCK, Christian
APPLICANT: BERLIN, Kurt
ITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ:
ITLE OF INVENTION: Cytosine methylation
ITLE OF INVENTION: Cytosine methylation
ITLE OF INVENTION UNMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR PELING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
SEQ ID NOS: 2424
LENGTH: 18997
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                                                                                                                                                                                                                                                                                                                                      19 ITGTAGTITGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGA
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                                                                                                                                                                                                                                                          Length 18997;
                                                                                                                                                                                          ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-172-086-17
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.2%; Score 60.4; DB 15; Best Local Similarity 49.7%; Pred. No. 0.78; Matches 154; Conservative 0; Mismatches 156;
                       CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 17
LENGTH: 18997
                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                 TYPE: DNA
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GENERAL INFORMATION:

APPLICANT: Nicholas M. Dean

APPLICANT: Nicholas M. Dean

TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPR

FILE REFERENCE: PTS-0011

CURRENT APPLICATION NUMBER: US/10/211,179

CURRENT FILING DATE: 2002-08-01

NUMBER OF SEQ ID NOS: 119

US-10-211-179-11
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4675 ATATTTATATATGIATTAGTTTATATTTÄTÄTÄTÄTGTTTATATATTTATTATA 4734
                                      67 AAAGATACTTGAAATAGCTTAGTTTAAATATAAAATAGCATAATAGATTTTAGGAATTAGT 126
                                                                                                                         127 ATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTAAATTCCAAGGCCCATGAAA 186
                                                                                                                                                                                                       187 AATITTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAAT 246
                                                                                                                                                                                                                                                                                           63 TAATAAAGATACTTGAAATAGCTTA---GTTTAAATATAAATAGCATAATAGATTTTAGG 119
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Publication No. US20030113750A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method and nucleic acids for the differentiation
TITLE OF INVENTION: Of prostate tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 17; Length 158001;
Pred. No. 1.2;
0; Mismatches 160; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                   307 CGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCA 347
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Matches 170; Conservative
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US-10-172-086-17
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                                                                                    13815 GATTTGTTTT 13824
                                                AGATTTATAT 328
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US-10-311-455-1542
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US-10-311-455-1549
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                                 TICAGGITITITITAATITITGIGGGATITITGATITIATATGITITITATIGAAATAATITGG 13574
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TTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGA
                                                                     AATAGCTTAGTTTAAATATATAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTA
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Sequence 31, Application US/10311507

Publication No. US20040115630A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: DEFENBROCK, Christian

APPLICANT: PIEPERBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE REFERENCE: 5013.1013

CURRENT APPLICATION NUMBER: US/10/311,507

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.2%; Score 60.4; DB 17;
Best Local Similarity 49.7%; Pred. No. 0.78;
Matches 154; Conservative 0; Mismatches 156;
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LENGTH: 18997
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Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION: US/10.11,455
                                                                                                                                                                                                                       Sequence 1549, Application US/10311455

Sequence 1549, Application US/10311455

Publication No. US2003014366A1

GENERAL INFORMATION:
APPLICANT: OLER, Alexander
TITLE OF INVENTION: Liagnosis of Diseases Associated with the Immune System by Deter
TITLE OF INVENTION: Liagnosis of Diseases Associated with the Immune System by PILE REFERENCE: 5013.1014

CURRENT APPLICATION WINBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 1549
2258
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0.59;
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Pred. No. 0.
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APPLICANT: BLUMELHELY, LYdie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: BTALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
CURRENT APPLICATION NUMBER: US 09/641,638
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2000-06-11
PRIOR PLICATION NUMBER: US 60/133,200
PRIOR PLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-23
PRIOR FILING DATE: 1999-03-23
PRIOR PLING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
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PRIOR APPLICATION NUMBER: US 60/119,917
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PRIOR APPLICATION NUMBER: US 60/119,917
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                                                                                                                                                                                                                                                                                                                                       124 AGTATITIGAGITITAATTACTIATIGACTIGIAACAGITITITATAATICCAAGGCCCAIG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4377 ATTATTTATTTTTGGAATTGTTTATTTTAATTTTTAGATTGTTATTGATTATGGGTAAT
                                                                                                                                          64 AATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                        184 AAAAATTTAATGCTTTATTAGTTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTT
                                                                             Gaps
                                                                             o;
      Length 5407;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 TATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTT 345
      Score 59.6; DB 15;
Pred. No. 0.73;
0; Mismatches 139;
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OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 651, Application US/10170097
Publication No. US20030228582A1
GENERAL INFORMATION:
      Query Match
Best Local Similarity 50.7%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blumenfeld, Marta
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OTHER INFORMATION: exon 3
FEATURE:
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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FEATURE:
NAME/KEY: misc_feature
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Sequence 2064, Application US/10311455

Publication No. US2003014366A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander

APPLICANT: PIPERNBROCK, Christian
APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT APPLICATION NUMBER: PCT/EP01/07537

PRIOR FILING DATE: 2001-07-02

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

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PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 ATTTAATGCTTTATTAGTTTTAAACTTACTATAAAATTTTTCATATGAAAATTTAATC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TATICAATACATHGTAGTTHGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 GGTACAGTTATAGATTTATATAAAATCTACGGTTCTTCAGAAGAAACCTAAAAAT 363
                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1542
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Pred. No. 0.71;
0; Mismatches 185; Indel8
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-09-01
SEQ ID NO 1542
LENGTH: 8305
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.0%;
Matches 171; Conservative
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US-10-311-455-2064
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NAME/KEY: exon LOCATION: 5996..6099 OTHER INFORMATION: exon 5

FEATURE:
NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6

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NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
                                                                                                                                                                                                                                                : polymorphic base A or G
                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or '
FEATURE:
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
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NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *FATURE:
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or
                                                                                 : polymorphic base G or C
                     FEATURE:
NAME/KEY: 311ele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
FEATURE:
NAME/KEY: 311ele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 6141
DTHER INFORMATION: 10-346-263 : polymorphic base G or
PEATURE:
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OTHER INFORMATION: 10-347-74 : polymorphic base A or
OTHER INFORMATION: 10-511-337 : insertion of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 :
FEATURE:
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305
FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: allele
COCATION: 2947
OTHER INFORMATION: 10-513-365
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ANME/KEX: allele
COCATION: 4088
THER INFORMATION: 12-206-366
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AME/KEY: allele
ACATION: 4109
DIHER INFORMATION: 10-343-278
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THER INFORMATION: 10-513-352
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NAME/KEY: allele
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NAME/KEY: allele
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OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTT
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
OCCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1559

THER INFORMATION: 10-509-284 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T FEATURE TO NAME/KEY: allele
LOCATION: 2323
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NAME/KEY: misc feature LOCATION: 17555..20674 OTHER INFORMATION: 3'regulatory region

NAME/KEY: exon LOCATION: 16567..16667 OTHER INFORMATION: exon 12

FEATURE: NAME/KEY: exon LOCATION: 16775..16945 OTHER INFORMATION: exon 13

NAME/KEY: exon LOCATION: 17063..17554 OTHER INFORMATION: exon 14

NAME/KEY: exon LOCATION: 13308..13429 )THER INFORMATION: exon 11 ?EATURE:

NAME/KEY: exon LOCATION: 12854..13023 OTHER INFORMATION: exon 10

NAME/KEY: exon LOCATION: 8645..8854 OTHER INFORMATION: exon 8

NAME/KEY: exon LOCATION: 7379..7522 OTHER INFORMATION: exon 7

NAME/KEY: exon LOCATION: 12254..12340 OTHER INFORMATION: exon 9

A 6.44.4 1.44.

: deletion of C

LOCATION: 1570 OTHER INFORMATION: 10-509-295 FEATURE: NAME/KEY: allele

FEATURE: NAME/KEY: allele

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GENERAL INFORMATION:

APPLICANT: Nicholas M. Dean

APPLICANT: Nicholas M. Dobia

TITLE OF INVERTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPR

FILE REFERENCE: PTS-0011

CURRENT APPLICATION NUMBER: US/10/211,179

CURRENT FILING DATE: 2002-08-01

NUMBER OF SEQ ID MOS: 119

OTHER INFORMATION: n = a, t, c, or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GATTTTAGGAATTAGTATTTTGAGTTTAATTACTTGACTTGTAACAGTTTTTATAAT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAATAAAGATACTTGAAATAGCTTA---GTTTAAATATAAATAGCATAATAGATTTTAGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 AACTTACCCTAATTATCGGTACAGTTATAGATTTATAAAAAATCTACGGTTCTTCAGAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATGTAAAATTTTAATCGGTATAGTTCGATATTTTTTTCAATTTATTATAAAATAAAA
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Pred. No. 1.2;
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LOCATION: 6467
OTHER INFORMATION: 10-347-203
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Search completed: August 3, 2004, 20:51:30 Job time : 347 secs